



PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/647,780A

DATE: 02/06/2002
TIME: 14:14:29

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\02062002\I647780A.raw

ENTERED

5 <110> APPLICANT: OUIMET et al.
 7 <120> TITLE OF INVENTION: Novel membrane-bound metalloprotease NEP II and the use thereof for
 8 screening inhibitors useful in therapy
 10 <130> FILE REFERENCE: P06910US0/BAS
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/647,780A
 C--> 13 <141> CURRENT FILING DATE: 2001-12-13
 15 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00807
 16 <151> PRIOR FILING DATE: 1999-04-07
 18 <150> PRIOR APPLICATION NUMBER: FR/9804389
 19 <151> PRIOR FILING DATE: 1998-04-08
 21 <160> NUMBER OF SEQ ID NOS: 29
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2765
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Rattus rattus
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (107) ... (2428)
 34 <400> SEQUENCE: 1
 35 gcaaaggact agcttcaagtg tgctcaaggc atccaaagctc cagctgcctc cctccctggcc 60
 37 ctggccctgg gtgctcaagct gtgtgccttc cacccagaac cggctg atg ggg aag 115
 38 Met Gly Lys
 39
 41 tcg gag agc tca gtg ggg atg atg gag aga gcg gac aac tgt ggg agg 163
 42 Ser Glu Ser Ser Val Gly Met Met Glu Arg Ala Asp Asn Cys Gly Arg
 43 5 10 15
 45 agg cgc cta ggc ttc gtg gag tgt ggg ctg ctg gta ctg ctg aca ctg 211
 46 Arg Arg Leu Gly Phe Val Glu Cys Gly Leu Leu Val Leu Leu Thr Leu
 47 20 25 30 35
 49 ctg ttg atg gga gcc ata gtg act ctg ggt gtc ttc tac agc ata ggg 259
 50 Leu Leu Met Gly Ala Ile Val Thr Leu Gly Val Phe Tyr Ser Ile Gly
 51 40 45 50
 53 aag cag ctg ccc ctc tta aat agc ctg ctg cac gtc tcc cgg cat gag 307
 54 Lys Gln Leu Pro Leu Leu Asn Ser Leu Leu His Val Ser Arg His Glu
 55 55 60 65
 57 agg acg gtt gta aaa cga gtc ctc aga gat tca tcg cag aag agt gac 355
 58 Arg Thr Val Val Lys Arg Val Leu Arg Asp Ser Ser Gln Lys Ser Asp
 59 70 75 80
 61 atc tgt act acc cca agc tgc gtg ata gca gct gcc aga atc ctc cag 403
 62 Ile Cys Thr Thr Pro Ser Cys Val Ile Ala Ala Arg Ile Leu Gln
 63 85 90 95
 65 aac atg gac cag tca aag aaa ccc tgc gac aac ttc tat cag tat gct 451

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66 Asn Met Asp Gln Ser Lys Lys Pro Cys Asp Asn Phe Tyr Gln Tyr Ala		
67 100 105 110 115		
69 tgc gga ggc tgg cta cg ^g cac cat gtg atc ccc gag acc aac tcc aga		499
70 Cys Gly Gly Trp Leu Arg His His Val Ile Pro Glu Thr Asn Ser Arg		
71 120 125 130		
73 tac agc gtc ttt gac atc ctt cg ^g gag ctg gag gtc atc ctc aaa		547
74 Tyr Ser Val Phe Asp Ile Leu Arg Asp Glu Leu Glu Val Ile Leu Lys		
75 135 140 145		
77 ggg gtg ctg gag gat tcc tct gtc cag cac cgc cca gct gtg gag aag		595
78 Gly Val Leu Glu Asp Ser Ser Val Gln His Arg Pro Ala Val Glu Lys		
79 150 155 160		
81 gcc aag aca ctg tac cgc tcc tgc atg aac cag agt gtg ata gag aag		643
82 Ala Lys Thr Leu Tyr Arg Ser Cys Met Asn Gln Ser Val Ile Glu Lys		
83 165 170 175		
85 aga gac tot gag ccc ctg ctg aac gtc tta gat atg ata gga ggt tgg		691
86 Arg Asp Ser Glu Pro Leu Leu Asn Val Leu Asp Met Ile Gly Gly Trp		
87 180 185 190 195		
89 cct gta gcc atg gac aag tgg aat gag acc atg ggc ccc aag tgg gaa		739
90 Pro Val Ala Met Asp Lys Trp Asn Glu Thr Met Gly Pro Lys Trp Glu		
91 200 205 210		
93 ctg gag cgg cag ttg gct gtg ttg aac tcg cag ttc aac agg cgc gtc		787
94 Leu Glu Arg Gln Leu Ala Val Leu Asn Ser Gln Phe Asn Arg Arg Val		
95 215 220 225		
97 ctc atc gac ctc ttc atc tgg aat gat gac cag aac tcc agc cgg cac		835
98 Leu Ile Asp Leu Phe Ile Trp Asn Asp Asp Gln Asn Ser Ser Arg His		
99 230 235 240		
101 gtc atc tac ata gac cag ccc acc ttg ggc atg ccc tcc cgg gag tac		883
102 Val Ile Tyr Ile Asp Gln Pro Thr Leu Gly Met Pro Ser Arg Glu Tyr		
103 245 250 255		
105 tat ttc aag gaa gac agc cac cgg gta cgg gaa gcc tac ctg cag ttc		931
106 Tyr Phe Lys Glu Asp Ser His Arg Val Arg Glu Ala Tyr Leu Gln Phe		
107 260 265 270 275		
109 atg aca tca gtg gcc act atg ctg agg aga gac ctg aac ctg ccc ggg		979
110 Met Thr Ser Val Ala Thr Met Leu Arg Arg Asp Leu Asn Leu Pro Gly		
111 280 285 290		
113 gag acc gat ttg gtg cag gag gaa atg gca cag gtg ctg cat ctg gag		1027
114 Glu Thr Asp Leu Val Gln Glu Glu Met Ala Gln Val Leu His Leu Glu		
115 295 300 305		
117 aca cat ctg gcc aac gcc acg gtc ccc cag gag aaa agg cat gat gtc		1075
118 Thr His Leu Ala Asn Ala Thr Val Pro Gln Glu Lys Arg His Asp Val		
119 310 315 320		
121 acc gcc ctg tat cac cga atg ggc ctg gag gag ctg cag gaa agg ttt		1123
122 Thr Ala Leu Tyr His Arg Met Gly Leu Glu Glu Leu Gln Glu Arg Phe		
123 325 330 335		
125 ggt ctg aag ggg ttt aac tgg act ctc ttc ata caa aac gtg ctg tct		1171
126 Gly Leu Lys Gly Phe Asn Trp Thr Leu Phe Ile Gln Asn Val Leu Ser		
127 340 345 350 355		
129 tct gtg caa gtt gag ctg ctc ccg aat gag gag gtg gtg gtc tat ggc		1219
130 Ser Val Gln Val Glu Leu Pro Asn Glu Glu Val Val Val Tyr Gly		

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131	360	365	370	
133	atc ccc tac ctg gag aat ctt gag gag atc att gac gtc ttc cca gca			1267
134	Ile Pro Tyr Leu Glu Asn Leu Glu Glu Ile Ile Asp Val Phe Pro Ala			
135	375	380	385	
137	cag acc ttg caa aac tac ctg gtg tgg cgc ctg gtg cta gat cgc atc			1315
138	Gln Thr Leu Gln Asn Tyr Leu Val Trp Arg Leu Val Leu Asp Arg Ile			
139	390	395	400	
141	ggc agc ctg agc cag aga ttc aaa gaa gcg cgt gtg gac tac cgc aag			1363
142	Gly Ser Leu Ser Gln Arg Phe Lys Glu Ala Arg Val Asp Tyr Arg Lys			
143	405	410	415	
145	gct ctg tac ggt aca acc atg gag gaa gta cgc tgg cgg gag tgt gtc			1411
146	Ala Leu Tyr Gly Thr Thr Met Glu Glu Val Arg Trp Arg Glu Cys Val			
147	420	425	430	435
149	agc tat gtc aac agc aac atg gag agt gcc gtg ggc tcc ctc tac atc			1459
150	Ser Tyr Val Asn Ser Asn Met Glu Ser Ala Val Gly Ser Leu Tyr Ile			
151	440	445	450	
153	aag cgg gcc ttc tcc aag gac agc aag agc ata gtc agt gag ctt atc			1507
154	Lys Arg Ala Phe Ser Lys Asp Ser Lys Ser Ile Val Ser Glu Leu Ile			
155	455	460	465	
157	gag aag ata cgg tcc gtg ttt gtg gat aac ctg gac gag ttg aac tgg			1555
158	Glu Lys Ile Arg Ser Val Phe Val Asp Asn Leu Asp Glu Leu Asn Trp			
159	470	475	480	
161	atg gat gag gaa tcc aag aaa aag gcc cag gaa aag gcc ttg aat atc			1603
162	Met Asp Glu Glu Ser Lys Lys Ala Gln Glu Lys Ala Leu Asn Ile			
163	485	490	495	
165	cgg gaa cag atc ggc tac cct gac tac att ttg gaa gac aat aac aga			1651
166	Arg Glu Gln Ile Gly Tyr Pro Asp Tyr Ile Leu Glu Asp Asn Asn Arg			
167	500	505	510	515
169	cac ctg gat gag gaa tac tcc agt ctg act ttc tca gag gac ctg tat			1699
170	His Leu Asp Glu Glu Tyr Ser Ser Leu Thr Phe Ser Glu Asp Leu Tyr			
171	520	525	530	
173	ttt gag aac ggg ctt cag aac ctc aag aac aat gcc caa agg agc ctc			1747
174	Phe Glu Asn Gly Leu Gln Asn Leu Lys Asn Asn Ala Gln Arg Ser Leu			
175	535	540	545	
177	aag aaa ctt cgg gaa aag gtg gac cag aat ctc tgg atc att ggg gct			1795
178	Lys Lys Leu Arg Glu Lys Val Asp Gln Asn Leu Trp Ile Ile Gly Ala			
179	550	555	560	
181	gca gtg gtc aat gca ttc tac tcc cca aac aga aac ctg atc gtc ttt			1843
182	Ala Val Val Asn Ala Phe Tyr Ser Pro Asn Arg Asn Leu Ile Val Phe			
183	565	570	575	
185	cca gcg ggg atc ctc cag cca ccc ttc agc aag gac caa cca cag			1891
186	Pro Ala Gly Ile Leu Gln Pro Pro Phe Phe Ser Lys Asp Gln Pro Gln			
187	580	585	590	595
189	gcc ttg aat ttc ggg ggc atc ggg atg gtg att gga cac gag atc aca			1939
190	Ala Leu Asn Phe Gly Gly Ile Gly Met Val Ile Gly His Glu Ile Thr			
191	600	605	610	
193	cac ggc ttt gat gat aac ggt cgg aac ttt gac aag aat ggc aac atg			1987
194	His Gly Phe Asp Asp Asn Gly Arg Asn Phe Asp Lys Asn Gly Asn Met			
195	615	620	625	

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197	ctg	gac	tgg	tgg	agc	aac	ttc	tcg	gcc	cg	cac	ttc	cga	cag	cag	tca	2035		
198	Leu	Asp	Trp	Trp	Ser	Asn	Phe	Ser	Ala	Arg	His	Phe	Arg	Gln	Gln	Ser			
199																630	635	640	
201	cag	tgt	atg	att	tat	cag	tac	agc	aac	ttc	tct	tgg	gaa	cta	gca	gac	2083		
202	Gln	Cys	Met	Ile	Tyr	Gln	Tyr	Ser	Asn	Phe	Ser	Trp	Glu	Leu	Ala	Asp			
203																645	650	655	
205	aac	cag	aat	gtg	aac	gga	ttc	agc	acc	ctc	gg	gag	aac	atc	gcc	gac	2131		
206	Asn	Gln	Asn	Val	Asn	Gly	Phe	Ser	Thr	Leu	Gly	Glu	Asn	Ile	Ala	Asp			
207																660	665	670	675
209	aac	ggc	gg	gtg	cg	g	cag	gca	tac	aag	gct	tac	cta	cag	tgg	cta	gct	2179	
210	Asn	Gly	Gly	Val	Arg	Gln	Ala	Tyr	Lys	Ala	Tyr	Leu	Gln	Trp	Leu	Ala			
211																680	685	690	
213	gaa	ggc	ggc	aga	gac	cag	aga	ctg	ccg	gga	ctg	aac	ctg	acc	tat	gct	2227		
214	Glu	Gly	Gly	Arg	Asp	Gln	Arg	Leu	Pro	Gly	Leu	Asn	Leu	Thr	Tyr	Ala			
215																695	700	705	
217	cag	ctt	ttc	ttc	att	aa	c	ttc	cag	gtg	tgg	tgt	gg	tcc	tac	agg	2275		
218	Gln	Leu	Phe	Phe	Ile	Asn	Tyr	Ala	Gln	Val	Trp	Cys	Gly	Ser	Tyr	Arg			
219																710	715	720	
221	ccg	gag	ttc	gcc	atc	cag	tcc	atc	aag	aca	gat	gtc	cac	agt	cct	ttt	2323		
222	Pro	Glu	Phe	Ala	Ile	Gln	Ser	Ile	Lys	Thr	Asp	Val	His	Ser	Pro	Leu			
223																725	730	735	
225	aag	ta	c	gg	gt	g	gc	t	ca	c	a	c	ta	cc	gg	tt	2371		
226	Lys	Tyr	Arg	Val	Leu	Gly	Ser	Leu	Gln	Asn	Leu	Pro	Gly	Phe	Ser	Glu			
227																740	745	750	755
229	g	cg	ttc	cac	tgc	cca	cga	gg	gc	ag	ccc	atg	cac	cct	atg	aat	2419		
230	Ala	Phe	His	Cys	Pro	Arg	Gly	Ser	Pro	Met	His	Pro	Met	Asn	Arg	Cys			
231																760	765	770	
233	cgc	atc	tgg	tagccaaggc	ttagctatgc	tgcggccac	gccccggcac										2468		
234	Arg	Ile	Trp																
237	ccagaggc	c	gtg	aat	gg	gt	tgcc	tt	tg	ca	gg	tt	tg	cc	ac	cc	2528		
239	tggagcc	acc	agcc	agcc	cc	c	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2588		
241	gat	tg	at	gt	gg	tg	ct	tg	cc	tt	cc	gg	cc	cc	cc	cc	2648		
243	gg	agc	ag	gt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2708		
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259						20				25						30			
261	Leu	Thr	Leu	Leu	Leu	Met	Gly	Ala	Ile	Val	Thr	Leu	Gly	Val	Phe	Tyr			
262						35				40						45			
264	Ser	Ile	Gly	Lys	Gln	Leu	Pro	Leu	Leu	Asn	Ser	Leu	Leu	His	Val	Ser			
265						50				55						60			
267	Arg	His	Glu	Arg	Thr	Val	Val	Lys	Arg	Val	Leu	Arg	Asp	Ser	Ser	Gln			
268						65				70						75			80

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270 Lys Ser Asp Ile Cys Thr Thr Pro Ser Cys Val Ile Ala Ala Ala Arg
 271 85 90 95
 273 Ile Leu Gln Asn Met Asp Gln Ser Lys Lys Pro Cys Asp Asn Phe Tyr
 274 100 105 110
 276 Gln Tyr Ala Cys Gly Gly Trp Leu Arg His His Val Ile Pro Glu Thr
 277 115 120 125
 279 Asn Ser Arg Tyr Ser Val Phe Asp Ile Leu Arg Asp Glu Leu Glu Val
 280 130 135 140
 282 Ile Leu Lys Gly Val Leu Glu Asp Ser Ser Val Gln His Arg Pro Ala
 283 145 150 155 160
 285 Val Glu Lys Ala Lys Thr Leu Tyr Arg Ser Cys Met Asn Gln Ser Val
 286 165 170 175
 288 Ile Glu Lys Arg Asp Ser Glu Pro Leu Leu Asn Val Leu Asp Met Ile
 289 180 185 190
 291 Gly Gly Trp Pro Val Ala Met Asp Lys Trp Asn Glu Thr Met Gly Pro
 292 195 200 205
 294 Lys Trp Glu Leu Glu Arg Gln Leu Ala Val Leu Asn Ser Gln Phe Asn
 295 210 215 220
 297 Arg Arg Val Leu Ile Asp Leu Phe Ile Trp Asn Asp Asp Gln Asn Ser
 298 225 230 235 240
 300 Ser Arg His Val Ile Tyr Ile Asp Gln Pro Thr Leu Gly Met Pro Ser
 301 245 250 255
 303 Arg Glu Tyr Tyr Phe Lys Glu Asp Ser His Arg Val Arg Glu Ala Tyr
 304 260 265 270
 306 Leu Gln Phe Met Thr Ser Val Ala Thr Met Leu Arg Arg Asp Leu Asn
 307 275 280 285
 309 Leu Pro Gly Glu Thr Asp Leu Val Gln Glu Glu Met Ala Gln Val Leu
 310 290 295 300
 312 His Leu Glu Thr His Leu Ala Asn Ala Thr Val Pro Gln Glu Lys Arg
 313 305 310 315 320
 315 His Asp Val Thr Ala Leu Tyr His Arg Met Gly Leu Glu Glu Leu Gln
 316 325 330 335
 318 Glu Arg Phe Gly Leu Lys Gly Phe Asn Trp Thr Leu Phe Ile Gln Asn
 319 340 345 350
 321 Val Leu Ser Ser Val Gln Val Glu Leu Leu Pro Asn Glu Glu Val Val
 322 355 360 365
 324 Val Tyr Gly Ile Pro Tyr Leu Glu Asn Leu Glu Glu Ile Ile Asp Val
 325 370 375 380
 327 Phe Pro Ala Gln Thr Leu Gln Asn Tyr Leu Val Trp Arg Leu Val Leu
 328 385 390 395 400
 330 Asp Arg Ile Gly Ser Leu Ser Gln Arg Phe Lys Glu Ala Arg Val Asp
 331 405 410 415
 333 Tyr Arg Lys Ala Leu Tyr Gly Thr Thr Met Glu Glu Val Arg Trp Arg
 334 420 425 430
 336 Glu Cys Val Ser Tyr Val Asn Ser Asn Met Glu Ser Ala Val Gly Ser
 337 435 440 445
 339 Leu Tyr Ile Lys Arg Ala Phe Ser Lys Asp Ser Lys Ser Ile Val Ser
 340 450 455 460
 342 Glu Leu Ile Glu Lys Ile Arg Ser Val Phe Val Asp Asn Leu Asp Glu

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date